

Amendments to the Specification:

Please modify the paragraphs at page 1, lines 13-27 in the following manner:

A conventional blood flow dynamic analyzing apparatus uses, for example, an X-ray CT apparatus to carry out dynamic imaging. During the imaging, an iodine-based contrast medium is injected into a patient. The blood flow dynamic analyzing apparatus thus provides information on a temporal variation in the concentration of the injected contrast medium. A time-concentration curve can be obtained from the temporal variation. Then, by analyzing the curve of the time-concentration curve, it is possible to obtain biological function information such as blood flow dynamics. Typical algorithms for analyzing the blood flow dynamics include a ~~gamma-fitting method~~ first moment method (gamma-fitting method), a maximum slope method, and a deconvolution method.

First, the ~~gamma-fitting method~~ first moment method (gamma-fitting method) uses a gamma function to approximate the time-concentration curve. Then, blood flow information is calculated from a peak value of the approximate curve and an area under the curve. Next, the maximum slope method calculates a blood flow by dividing the maximum value of slope of the time-concentration curve for each tissue by the maximum value of a rise in a CT value in an arterial input function.

Please modify the paragraph at page 1, line 28 through page 2, line 2 in the following manner:

However, the ~~gamma-fitting method~~ first moment method (gamma-fitting method) and the maximum slope method require that about 8 to 10 ml/sec of contrast medium be injected into the subject. Disadvantageously, this is a heavy burden on the physical strength of the subject into which the contrast medium is injected. Moreover, disadvantageously, the

gamma fitting method enables qualitative evaluation but not quantitative evaluation.

Please modify the paragraph at page 2, lines 3-12 in the following manner:

Thus, efforts were made to develop a blood flow analyzing method which can reduce the contrast rate and which enables quantitative evaluation. As a result, the deconvolution method has been proposed (see the well-known document shown below). The deconvolution method subjects an arterial input function and a tissue ~~residue~~ output function to deconvolution to generate an impulse residue function. Then, blood flow information is calculated from a peak value or an area under the curve of the impulse residue function generated. The deconvolution method advantageously enables examinations at a low contrast rate of about 3 to 5 ml/sec. Accordingly, the deconvolution method requires a contrast medium injection speed that is only about half that of the ~~gamma-fitting method~~ first moment method (gamma-fitting method) or the maximum slope method.

Please modify the paragraph at page 2, lines 16-19 in the following manner:

However, the deconvolution method requires a plurality of integrations in the data conversion calculation that determines the impulse residue function from the arterial input function and tissue ~~residue~~ output function. Consequently, the deconvolution method requires a time for the calculation.

Please modify the paragraph at page 17, lines 5-13 in the following manner:

As described above, according to the above embodiment, if biological function information analysis is to be executed on a tomogram dynamically acquired using a computer

tomogram diagnosing apparatus, the analysis can be accomplished with a contrast rate lower than that of the ~~gamma-fitting method~~ first moment method (gamma-fitting method) or maximum slope method and with a calculation time shorter than that of the deconvolution method. The embodiment is also effective in preventing the degradation of quantitiveness attributed to the PVA effect. The embodiment is also effective in preventing an unnecessary increase in calculation time owing to unwanted areas and analysis precision without increasing a burden on the operator.